

17. (New) The method of Claim 16, wherein the similarity between the selected peptide and the plurality of database peptides comprises determination of a plurality of mass score values, each of which are associated with a particular database peptide and are determined by evaluating the similarity between the query mass set with the associated mass sets.

18. (New) The method of Claim 17, wherein the database peptide having the highest mass score value is determined to be analogous to the selected peptide.

19. (New) The method of Claim 17, wherein a tolerance value is further assessed in conjunction with the mass score value thereby providing flexibility in matching the query mass set to the associated mass sets.

20. (New) The method of Claim 16, wherein the mass score values for the database peptides and the selected peptide are based upon mass spectroscopic analysis.

21. (New) The method of Claim 20, wherein said mass spectroscopic analysis is performed by a method selected from the group consisting of: Fourier transform ion cyclotron resonance ("FTICR"), quadrupole mass spectroscopy, ion trap mass spectroscopy, and time-of-flight mass spectroscopy.

22. (New) The method of Claim 17, wherein a weighting value is assessed in conjunction with the mass score value wherein the weighting value is defined according to a peptide fragment ion type reflected by the mass score value.

23. (New) The method of Claim 22, wherein the peptide fragment ion type is selected from the group consisting of: y-ions, b-ions, a-ions and immonium ions.

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24. (New) The method of Claim 17, wherein a weighting value is assessed in conjunction with the mass score value wherein the weighting value is defined according to a peptide fragment characteristic reflected by the mass value.

25. (New) The method of Claim 24, wherein the peptide fragment characteristic is selected from the group consisting of: peak mass, complementary mass, fragment charge, and mass ratio.

26. (New) The method of Claim 16, wherein when performing the search of the index table, putative peptide modifications are evaluated based on a predicted mass associated with the putative peptide modification that contributes to either the database peptide masses or the selected peptide mass.

27. (New) The method of Claim 26, wherein the putative peptide modifications comprise modifications selected from the group consisting of: post-translational modifications, phosphorylation, glycosylation, and substitutions.

28. (New) The method of Claim 26, wherein comparison of the query mass set with the associated mass set is performed in conjunction with evaluating putative peptide modifications to account for differences between the mass of the selected peptide with the database peptides.

29. (New) A method for comparing a modified query peptide to a plurality of database peptides comprising:

identifying a plurality of associated mass values for the plurality of database peptides wherein the associated mass values reflect peptide ion mass fragment information comprising parent and progeny ion fragments;

generating a plurality of query mass values for a query peptide wherein the query mass values reflect peptide ion mass fragment information comprising parent and progeny ion fragments;